

SEQUENCE LISTING

<110> Brett P. Monia
Susan M. Freier
Scott Cooper

<120> ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2
EXPRESSION

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<213> Homo sap

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ttgcgcgtag tccatgcccg tagaggaagt gtgcagatgg gattaacgtc cacatggaga 240
tatggaagag gaccggggat tggtagcgta acc atg gtc agc tgg ggt cgt ttc 294
Met Val Ser Trp Gly Arg Phe
1 5

atc tgc ctg gtc gtg gtc acc atg gca acc ttg tcc ctg gcc cgg ccc 342
Ile Cys Leu Val Val Val Thr Met Ala Thr Leu Ser Leu Ala Arg Pro
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tcc ttc agt tta gtt gag gat acc aca tta gag cca gaa gag cca cca 390
Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu Pro Pro
25 30 35

acc aaa tac caa atc tct caa cca gaa gtg tac gtg gct gcg cca ggg 438
Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala Pro Gly
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gag tcg cta gag gtg cgc tgc ctg ttg aaa gat gcc gcc gtg atc a 56
Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val Ile
60 65 70 75 80 85 90

tgg act aag gat ggg gtg cac ttg ggg ccc aac aat 534
Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asp tcc ggc
75 80 85 90 95 100 105 110 115 120

att ggg gag tac ttg cag ata aag ggc 582
Ile Gly Glu Tyr Leu Gln Ile Lys Cys
90 95 100 105 110 115 120

ctc tat gct tgt act gcc agt agg act gta gac agt gaa act tgg tac 630
 Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr Trp Tyr
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ttc atg gtg aat gtc aca gat gcc atc tca tcc gga gat gat gag gat 678
 Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp
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gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac aag 726
 Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys
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aga gca cca tac tgg acc aac aca gaa aag atg gaa aag cgg ctc cat 774
 Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His
 155 160 165

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 Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly
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 Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys
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 Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser
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 Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp
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 Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro
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 Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys
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 Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu
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 Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val
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 315 320 325

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 Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu
 330 335 340

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 Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu Thr Val
 345 350 355

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 360 365 370 375

ctg gag ata gcc att tac tgc ata ggg gtc ttc tta atc gcc tgt atg 1446
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 380 385 390

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 395 400 405

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 Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro
 410 415 420

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 Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn
 425 430 435

tcc aac acc ccg ctg gtg agg ata aca aca cgc ctc tct tca acg gca 1638
 Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala
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Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile	
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Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu	
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Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met	
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Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala	
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Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly	
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Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn	
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Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly	
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Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val	
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Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg	
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Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr Glu Pro	
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Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
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Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Leu Val Thr	
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Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp	
15 20 25 30	
acc act tta gaa cca gaa gag cca cca acc aaa tac caa atc tcc caa	744

Thr Thr Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln
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 cca gaa gcg tac gtg gtt gcc ccc ggg gaa tcg cta gag ttg cag tgc 792
 Pro Glu Ala Tyr Val Val Ala Pro Gly Glu Ser Leu Glu Leu Gln Cys
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 Met Leu Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His
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 aaa ggt gcc aca cct aga gac tcc ggc ctc tat gct tgt act gca gct 936
 Lys Gly Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ala
 95 100 105 110
 agg acg gta gac agt gaa act tgg atc ttc atg gtg aat gtc aca gat 984
 Arg Thr Val Asp Ser Glu Thr Trp Ile Phe Met Val Asn Val Thr Asp
 115 120 125
 gcc atc tca tct gga gat gat gag gac gac aca gat agc tcc gaa gac 1032
 Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Ser Ser Glu Asp
 130 135 140
 gtt gtc agt gag aac agg agc aac cag aga gca ccg tac tgg acc aac 1080
 Val Val Ser Glu Asn Arg Ser Asn Gln Arg Ala Pro Tyr Trp Thr Asn
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 acc gag aag atg gag aag cgg ctc cac gct tgt cct gcc gcc aac act 1128
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 Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro Thr Ser Thr Met Arg
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 Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly
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 255 260 265 270

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 Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro
 275 280 285

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 His Ile Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Asn Gly
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 Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn
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 355 360 365

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Ile Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Phe Cys
 385 390 395

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 Arg Met Lys Thr Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala
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 415 420 425 430

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 435 440 445

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 Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly
 450 455 460

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 465 470 475

gat aag ctg acg ctg ggc aaa ccc ctg ggg gaa ggt tgc ttc ggg caa 2088
 Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln
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 495 500 505 510

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 545 550 555

cct ctc tac gtc ata gtt gaa tat gca tcg aaa ggc aac ctc cgg gaa 2328

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Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile	
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Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys	
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acc tac cag ctg gct aga ggc atg gag tac ttg gct tcc caa aaa tgt	2472
Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys	
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 Department of
 Commerce
 Washington, D.C. 20540

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Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu			
	145	150	155
aag atg gaa aag cgg ctc cat gct gtg cct gcg gcc aac act gtc aag			946
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys			
	165	170	175
ttt cgc tgc cca gcc ggg ggg aac cca atg cca acc atg cgg tgg ctg			994
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu			
	180	185	190
aaa aac ggg aag gag ttt aag cag gag cat cgc att gga ggc tac aag			1042
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys			
	195	200	205
gta cga aac cag cac tgg agc ctc att atg gaa agt gtg gtc cca tct			1090
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser			

210	215	220	
gac aag gga aat tat acc tgt gta gtg gag aat gaa tac ggg tcc atc			1138
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile			
225	230	235	240
aat cac acg tac cac ctg gat gtt gtg gag cga tcg cct cac cgg ccc			1186
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro			
245	250	255	
atc ctc caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc gga gga			1234
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly			
260	265	270	
gac gta gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc cac atc			1282
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile			
275	280	285	
cag tgg atc aag cac gtg gaa aag aac ggc agt aaa tac ggg ccc gac			1330
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp			
290	295	300	
ggg ctg ccc tac ctc aag gtt ctc aag cac tcg ggg ata aat agt tcc			1378
Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser			
305	310	315	320
aat gca gaa gtg ctg gct ctg ttc aat gtg acc gag gcg gat gct ggg			1426
Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly			
325	330	335	
gaa tat ata tgt aag gtc tcc aat tat ata ggg cag gcc aac cag tct			1474
Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser			
340	345	350	
gcc tgg ctc act gtc ctg cca aaa cag caa gcg cct gga aga gaa aag			1522
Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys			
355	360	365	
gag att aca gct tcc cca gac tac ctg gag ata gcc att tac tgc ata			1570
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile			
370	375	380	
ggg gtc ttc tta atc gcc tgt atg gtg gta aca gtc atc ctg tgc cga			1618
Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg			

385	390	395	400	
atg aag aac acg acc aag aag cca gac ttc agc agc cag ccg gct gtg				1666
Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val				
	405	410	415	
cac aag ctg acc aaa cgt atc ccc ctg cgg aga cag gta aca gtt tcg				1714
His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser				
	420	425	430	
gct gag tcc agc tcc tcc atg aac tcc aac acc ccg ctg gtg agg ata				1762
Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile				
	435	440	445	
aca aca cgc ctc tct tca acg gca gac acc ccc atg ctg gca ggg gtc				1810
Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val				
	450	455	460	
tcc gag tat gaa ctt cca gag gac cca aaa tgg gag ttt cca aga gat				1858
Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp				
	465	470	475	480
aag ctg aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg				1906
Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val				
	485	490	495	
gtc atg gcg gaa gca gtg gga att gac aaa gac aag ccc aag gag gcg				1954
Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala				
	500	505	510	
gtc acc gtg gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac				2002
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp				
	515	520	525	
ctt tct gat ctg gtg tca gag atg gag atg atg aag atg att ggg aaa				2050
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys				
	530	535	540	
cac aag aat atc ata aat ctt ctt gga gcc tgc aca cag gat ggg cct				2098
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro				
	545	550	555	560
ctc tat gtc ata gtt gag tat gcc tct aaa ggc aac ctc cga gaa tac				2146
Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr				

565	570	575	
ctc' cga gcc cgg agg cca ccc ggg atg gag tac tcc tat gac att aac			2194
Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn			
580	585	590	
cgt gtt cct gag gag cag atg acc ttc aag gac ttg gtg tca tgc acc			2242
Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr			
595	600	605	
tac cag ctg gcc aga cgg atg gag tac ttg gct tcc caa aaa tgt att			2290
Tyr Gln Leu Ala Arg Arg Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile			
610	615	620	
cat cga gat tta gca gcc aga aat gtt ttg gta aca gaa aac aat gtg			2338
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val			
625	630	635	640
atg aaa ata gca gac ttt gga ctc gcc aga gat atc aac aat ata gac			2386
Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp			
645	650	655	
tat tac aaa aag acc acc aat ggg cgg ctt cca gtc aag tgg atg gct			2434
Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala			
660	665	670	
cca gaa gcc ctg ttt gat aga gta tac act cat cag agt gat gtc tgg			2482
Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp			
675	680	685	
tcc ttc ggg gtg tta atg tgg gag atc ttc act tta ggg ggc tcg ccc			2530
Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro			
690	695	700	
tac cca ggg att ccc gtg gag gaa ctt ttt aag ctg ctg aag gaa gga			2578
Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly			
705	710	715	720
cac aga atg gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg			2626
His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met			
725	730	735	
atg agg gac tgt tgg cat gca gtg ccc tcc cag aga cca acg ttc aag			2674
Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys			

740 745 750
 cag ttg gta gaa gac ttg gat cga att ctc act ctc aca acc aat gag 2722
 Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
 755 760 765
 taa agccaaggat atgggagggg aaaaaagggg aaagagtcac ggaaagccag 2775

 cttcttgctg aaactccact aggtgccctg ctggaatctc ccttgaaaga g 2826

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 <213> Homo sapiens

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 <222> (1)...(99)

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 1 5 10 15
 ctc agt cag cct ctc gaa ccg tat tca cct tgt tat cct gac cca aga 96
 Leu Ser Gln Pro Leu Glu Pro Tyr Ser Pro Cys Tyr Pro Asp Pro Arg
 20 25 30
 tga aataaaacgt ctctcttccc ttctttcagg aatacttgga cctcagccaa 149

 cctctcgaac agtattcacc tagttaccct gacacaagaa gttcttggtc ttcaggagat 209
 gattctgttt tttctccaga ccccatgcct tacgaaccat gccttcctca gtatccacac 269
 ataaacggca gtgttaaaac atgaatgact gtgtctgcct g 310

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 <211> 3025
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 <213> Homo sapiens

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<220>

<221> CDS

<222> (595) ... (2643)

<400> 23

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cggcgtacct ggcccggcgc ggcgactgct ctccgggctg gcggggggccg gccgcgagcc      120

ccggggggccc cgaggccgca gcttgccctgc gcgctctgag ccttcgcaac tcgcgagcaa      180

agtttggtgg aggcaacgcc aagcctgagt cctttcttcc tctcgttccc caaatccgag      240

ggcagccccgc gggcgtcatg cccgcgctcc tccgcagcct ggggtacgcg tgaagcccgg      300

gaggcttggc gccggcgaag acccaaggac cactcttctg cgtttggagt tgctccccac      360

aaccgcgggc tcgtcgcttt ctccatcccg acccacgcgg ggcgcgggga caacacaggt      420

cgcgaggag cgttgccatt caagtgactg cagcagcagc ggcagcgcct cggttcctga      480

gcccaccgca ggctgaaggc attgcgcgta gtccatgccc gtagaggaag tgtgcagatg      540

ggattaacgt ccacatggag atatggaaga ggaccgggga ttggtaccgt aacc atg      597
                                     Met
                                     1

gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc atg gca acc      645
Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala Thr
          5              10              15

ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag gat acc aca tta      693
Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu
          20              25              30

gag cca gaa gat gcc atc tca tcc gga gat gat gag gat gac acc gat      741
Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp

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35	40	45	
ggt gcg gaa gat ttt gtc agt gag aac agt aac aac aag aga gca cca			789
Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro			
50	55	60	65
tac tgg acc aac aca gaa aag atg gaa aag cgg ctc cat gct gtg cct			837
Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val Pro			
70	75	80	
gcg gcc aac act gtc aag ttt cgc tgc cca gcc ggg ggg aac cca atg			885
Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro Met			
85	90	95	
cca acc atg cgg tgg ctg aaa aac ggg aag gag ttt aag cag gag cat			933
Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu His			
100	105	110	
cgc att gga ggc tac aag gta cga aac cag cac tgg agc ctc att atg			981
Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile Met			
115	120	125	
gaa agt gtg gtc cca tct gac aag gga aat tat acc tgt gtg gtg gag			1029
Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val Glu			
130	135	140	145
aat gaa tac ggg tcc atc aat cac acg tac cac ctg gat gtt gtg gag			1077
Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val Glu			
150	155	160	
cga tcg cct cac cgg ccc atc ctc caa gcc gga ctg ccg gca aat gcc			1125
Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala			
165	170	175	
tcc aca gtg gtc gga gga gac gta gag ttt gtc tgc aag gtt tac agt			1173
Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr Ser			
180	185	190	
gat gcc cag ccc cac atc cag tgg atc aag cac gtg gaa aag aac ggc			1221
Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn Gly			
195	200	205	
agt aaa tac ggg ccc gac ggg ctg ccc tac ctc aag gtt ctc aag cac			1269
Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys His			

210	215	220	225	
tcg ggg ata aat agt tcc aat gca gaa gtg ctg gct ctg ttc aat gtg				1317
Ser Gly Ile Asn Ser Ser Asn Ala Glu Val Leu Ala Leu Phe Asn Val				
	230	235	240	
acc gag gcg gat gct ggg gaa tat ata tgt aag gtc tcc aat tat ata				1365
Thr Glu Ala Asp Ala Gly Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile				
	245	250	255	
ggg cag gcc aac cag tct gcc tgg ctc act gtc ctg cca aaa cag caa				1413
Gly Gln Ala Asn Gln Ser Ala Trp Leu Thr Val Leu Pro Lys Gln Gln				
	260	265	270	
gcg cct gga aga gaa aag gag att aca gct tcc cca gac tac ctg gag				1461
Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu				
	275	280	285	
ata gcc att tac tgc ata ggg gtc ttc tta atc gcc tgt atg gtg gta				1509
Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val Val				
	290	295	300	305
aca gtc atc ctg tgc cga atg aag aac acg acc aag aag cca gac ttc				1557
Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp Phe				
	310	315	320	
agc agc cag ccg gct gtg cac aag ctg acc aaa cgt atc ccc ctg cgg				1605
Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu Arg				
	325	330	335	
aga cag gtt tcg gct gag tcc agc tcc tcc atg aac tcc aac acc ccg				1653
Arg Gln Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro				
	340	345	350	
ctg gtg agg ata aca aca cgc ctc tct tca acg gca gac acc ccc atg				1701
Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met				
	355	360	365	
ctg gca ggg gtc tcc gag tat gaa ctt cca gag gac cca aaa tgg gag				1749
Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu				
	370	375	380	385
ttt cca aga gat aag ctg aca ctg ggc aag ccc ctg gga gaa ggt tgc				1797
Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys				

	390	395	400	
ttt ggg caa gtg gtc atg gcg gaa gca gtg gga att gac aaa gac aag				1845
Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys				
	405	410	415	
ccc aag gag gcg gtc acc gtg gcc gtg aag atg ttg aaa gat gat gcc				1893
Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala				
	420	425	430	
aca gag aaa gac ctt tct gat ctg gtg tca gag atg gag atg atg aag				1941
Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys				
	435	440	445	
atg att ggg aaa cac aag aat atc ata aat ctt ctt gga gcc tgc aca				1989
Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr				
	450	455	460	465
cag gat ggg cct ctc tat gtc ata gtt gag tat gcc tct aaa ggc aac				2037
Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn				
	470	475	480	
ctc cga gaa tac ctc cga gcc cgg agg cca ccc ggg atg gag tac tcc				2085
Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser				
	485	490	495	
tat gac att aac cgt gtt cct gag gag cag atg acc ttc aag gac ttg				2133
Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu				
	500	505	510	
gtg tca tgc acc tac cag ctg gcc aga ggc atg gag tac ttg gct tcc				2181
Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser				
	515	520	525	
caa aaa tgt att cat cga gat tta gca gcc aga aat gtt ttg gta aca				2229
Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr				
	530	535	540	545
gaa aac aat gtg atg aaa ata gca gac ttt gga ctc gcc aga gat atc				2277
Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile				
	550	555	560	
aac aat ata gac tat tac aaa aag acc acc aat ggg cgg ctt cca gtc				2325
Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val				

565	570	575	
aag tgg atg gct cca gaa gcc ctg ttt gat aga gta tac act cat cag			2373
Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln			
580	585	590	
agt gat gtc tgg tcc ttc ggg gtg tta atg tgg gag atc ttc act tta			2421
Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu			
595	600	605	
ggg ggc tcg ccc tac cca ggg att ccc gtg gag gaa ctt ttt aag ctg			2469
Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu			
610	615	620	625
ctg aag gaa gga cac aga atg gat aag cca gcc aac tgc acc aac gaa			2517
Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu			
630	635	640	
ctg tac atg atg atg agg gac tgt tgg cat gca gtg ccc tcc cag aga			2565
Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg			
645	650	655	
cca acg ttc aag cag ttg gta gaa gac ttg gat cga att ccc ccc aac			2613
Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Pro Pro Asn			
660	665	670	
cct tcc ctt atg agc att ttt aga aaa tag tcttagccaa tgttctaaaa			2663
Pro Ser Leu Met Ser Ile Phe Arg Lys			
675	680		
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caacgggaac ttggatggat acagtctggg cctgctgggc cagatgttcc gagggcggcc			2783
cggcaagcag cctgtcttgc acattgcaac tgactggcctt aatctacggc aagagtcctt			2843
cagctccgtc acagagtact ctccaatgtg ttatagttat ccttaaagct cttcaattca			2903
aggaagtgct tggcacgttt actcttctga ctggagggga ggtatgtcac ctggatggtt			2963
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gg			3025

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 aagtgtgcag atgggattaa cgtccacatg gagatatgga agaggaccgg ggattggtac 480
 cgtaacc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc 529
 Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr
 1 5 10
 atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag gat 577
 Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp
 15 20 25 30
 acc aca tta gag cca gaa gag cca cca acc aaa tac caa atc tct caa 625
 Thr Thr Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln
 35 40 45
 cca gaa gtg tac gtg gct gcg cca ggg gag tcg cta gag gtg cgc tgc 673
 Pro Glu Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys
 50 55 60

ctg ttg aaa gat gcc gcc gtg atc agt tgg act aag gat ggg gtg cac 721
 Leu Leu Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His
 65 70 75

ttg ggg ccc aac aat agg aca gtg ctt att ggg gag tac ttg cag ata 769
 Leu Gly Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile
 80 85 90

aag ggc gcc acg cct aga gac tcc ggc ctc tat gct tgt act gcc agt 817
 Lys Gly Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser
 95 100 105 110

agg act gta gac agt gaa act tgg tac ttc atg gtg aat gtc aca gat 865
 Arg Thr Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp
 115 120 125

gcc atc tca tcc gga gat gat gag gat gac acc gat ggt gcg gaa gat 913
 Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp
 130 135 140

ttt gtc agt gag aac agt aac aac aag aga gca cca tac tgg acc aac 961
 Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn
 145 150 155

aca gaa aag atg gaa aag cgg ctc cat gct gtg cct gcg gcc aac act 1009
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 160 165 170

gtc aag ttt cgc tgc cca gcc ggg ggg aac cca atg cca acc atg cgg 1057
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 175 180 185 190

tgg ctg aaa aac ggg aag gag ttt aag cag gag cat cgc att gga ggc 1105
 Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly
 195 200 205

tac aag gta cga aac cag cac tgg agc ctc att atg gaa agt gtg gtc 1153
 Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val
 210 215 220

cca tct gac aag gga aat tat acc tgt gtg gtg gag aat gaa tac ggg 1201
 Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly
 225 230 235

tcc atc aat cac acg tac cac ctg gat gtt gtg gag cga tcg cct cac	1249
Ser Ile Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His	
240 245 250	
cgg ccc atc ctc caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc	1297
Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val	
255 260 265 270	
gga gga gac gta gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc	1345
Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro	
275 280 285	
cac atc cag tgg atc aag cac gtg gaa aag aac ggc agt aaa tac ggg	1393
His Ile Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly	
290 295 300	
ccc gac ggg ctg ccc tac ctc aag gtt ctc aag gtt tcg gct gag tcc	1441
Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys Val Ser Ala Glu Ser	
305 310 315	
agc tcc tcc atg aac tcc aac acc ccg ctg gtg agg ata aca aca cgc	1489
Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg	
320 325 330	
ctc tct tca acg gca gac acc ccc atg ctg gca ggg gtc tcc gag tat	1537
Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr	
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gaa ctt cca gag gac cca aaa tgg gag ttt cca aga gat aag ctg aca	1585
Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr	
355 360 365	
ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg gtc atg gcg	1633
Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala	
370 375 380	
gaa gca gtg gga att gac aaa gac aag ccc aag gag gcg gtc acc gtg	1681
Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val	
385 390 395	
gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac ctt tct gat	1729
Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp	
400 405 410	

att ccc gtg gag gaa ctt ttt aag ctg ctg aag gaa gga cac aga atg 2305
 Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met
 595 600 605

gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg atg agg gac 2353
 Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp
 610 615 620

tgt tgg cat gca gtg ccc tcc cag aga cca acg ttc aag cag ttg gta 2401
 Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val
 625 630 635

gaa gac ttg gat cga att ctc act ctc aca acc aat gag gaa tac ttg 2449
 Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu
 640 645 650

gac ctc agc caa cct ctc gaa cag tat tca cct agt tac cct gac aca 2497
 Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr
 655 660 665 670

aga agt tct tgt tct tca gga gat gat tct gtt ttt tct cca gac ccc 2545
 Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro
 675 680 685

atg cct tac gaa cca tgc ctt cct cag tat cca cac ata aac ggc agt 2593
 Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser
 690 695 700

gtt aaa aca tga atgactgtgt ctgcctgtcc ccaaacagga cagcactggg 2645
 Val Lys Thr
 705

aacctagcta cactgagcag ggagaccatg cctcccagag cttgttgtct ccacttgtat 2705

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agttgaaaac ttgtaatctt ccccaggagg agaagaaggt ttctggagca gtggactgcc 2825

acaagccacc atgtaacccc tctcacctgc cgtgcgttct ggctgtggac cagtaggact 2885

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<211> 3080

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<213> Homo sapiens

<220>

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<221> CDS

<222> (612)...(3080)

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gggcccggcg cgagccccgg gggccccgag gccgcagctt gcctgcgcgc tctgagcctt 180

cgcaactcgc gagcaaagtt tggtaggagg aacgccaaag ctgagtcctt tcttctcttc 240

gttccccaaa tccgagggca gccgcggggc gtcattgccg cgctcctccg cagcctgggg 300

tacgcgctga agcccgggag gcttggcgcc ggccaagacc caaggaccac tcttctgcgt 360

ttggagttgc tccccacaac cccgggctcg tcgctttctc catcccgacc cagccggggc 420

gcgggggacaa cacaggtcgc ggaggagcgt tgccattcaa gtgactgcag cagcagcggc 480

agcgcctcgg ttcctgagcc caccgcaggc tgaaggcatt gcgcgtagtc catgcccgta 540

gaggaagtgt gcagatggga ttaacgtcca catggagata tggaagagga ccggggattg 600

gtaccgtaac c atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc 650
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val

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acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag			698
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu			
15	20	25	
gat acc aca tta gag cca gaa gag cca cca acc aaa tac caa atc tct			746
Asp Thr Thr Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser			
30	35	40	45
caa cca gaa gtg tac gtg gct gcg cca ggg gag tcg cta gag gtg cgc			794
Gln Pro Glu Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg			
50	55	60	
tgc ctg ttg aaa gat gcc gcc gtg atc agt tgg act aag gat ggg gtg			842
Cys Leu Leu Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val			
65	70	75	
cac ttg ggg ccc aac aat agg aca gtg ctt att ggg gag tac ttg cag			890
His Leu Gly Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln			
80	85	90	
ata aag ggc gcc acg cct aga gac tcc ggc ctc tat gct tgt act gcc			938
Ile Lys Gly Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala			
95	100	105	
agt agg act gta gac agt gaa act tgg tac ttc atg gtg aat gtc aca			986
Ser Arg Thr Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr			
110	115	120	125
gat gcc atc tca tcc gga gat gat gag gat gac acc gat ggt gcg gaa			1034
Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu			
130	135	140	
gat ttt gtc agt gag aac agt aac aac aag aga gca cca tac tgg acc			1082
Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr			
145	150	155	
aac aca gaa aag atg gaa aag cgg ctc cat gct gtg cct gcg gcc aac			1130
Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn			
160	165	170	
act gtc aag ttt cgc tgc cca gcc ggg ggg aac cca atg cca acc atg			1178
Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met			

175	180	185	
cgg tgg ctg aaa aac ggg aag gag ttt aag cag gag cat cgc att gga			1226
Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly			
190	195	200	205
ggc tac aag gta cga aac cag cac tgg agc ctc att atg gaa agt gtg			1274
Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val			
210	215	220	
gtc cca tct gac aag gga aat tat acc tgt gtg gtg gag aat gaa tac			1322
Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr			
225	230	235	
ggg tcc atc aat cac acg tac cac ctg gat gtt gtg gag cga tcg cct			1370
Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro			
240	245	250	
cac cgg ccc atc ctc caa gcc gga ctg ccg gca aat gcc tcc aca gtg			1418
His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val			
255	260	265	
gtc gga gga gac gta gag ttt gtc tgc aag gtt tac agt gat gcc cag			1466
Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln			
270	275	280	285
ccc cac atc cag tgg atc aag cac gtg gaa aag aac ggc agt aaa tac			1514
Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr			
290	295	300	
ggg ccc gac ggg ctg ccc tac ctc aag gtt ctc aag cac tcg ggg ata			1562
Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile			
305	310	315	
aat agt tcc aat gca gaa gtg ctg gct ctg ttc aat gtg acc gag gcg			1610
Asn Ser Ser Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala			
320	325	330	
gat gct ggg gaa tat ata tgt aag gtc tcc aat tat ata ggg cag gcc			1658
Asp Ala Gly Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala			
335	340	345	
aac cag tct gcc tgg ctc act gtc ctg cca aaa cag caa gcg cct gga			1706
Asn Gln Ser Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly			

350	355	360	365	
aga gaa aag gag att aca gct tcc cca gac tac ctg gag ata gcc att				1754
Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile				
	370	375	380	
tac tgc ata ggg gtc ttc tta atc gcc tgt atg gtg gta aca gtc atc				1802
Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile				
	385	390	395	
ctg tgc cga atg aag aac acg acc aag aag cca gac ttc agc agc cag				1850
Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln				
	400	405	410	
ccg gct gtg cac aag ctg acc aaa cgt atc ccc ctg cgg aga cag gta				1898
Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val				
	415	420	425	
aca gtt tcg gct gag tcc agc tcc tcc atg aac tcc aac acc ccg ctg				1946
Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu				
	430	435	440	445
gtg agg ata aca aca cgc ctc tct tca acg gca gac acc ccc atg ctg				1994
Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu				
	450	455	460	
gca ggg gtc tcc gag tat gaa ctt cca gag gac cca aaa tgg gag ttt				2042
Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe				
	465	470	475	
cca aga gat aag ctg aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt				2090
Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe				
	480	485	490	
ggg caa gtg gtc atg gcg gaa gca gtg gga att gac aaa gac aag ccc				2138
Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro				
	495	500	505	
aag gag gcg gtc acc gtg gcc gtg aag atg ttg aaa gat gat gcc aca				2186
Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr				
	510	515	520	525
gag aaa gac ctt tct gat ctg gtg tca gag atg gag atg atg aag atg				2234
Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met				

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att ggg aaa cac aag aat atc ata aat ctt ctt gga gcc tgc aca cag			2282
Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln			
545	550	555	
gat ggg cct ctc tat gtc ata gtt gag tat gcc tct aaa ggc aac ctc			2330
Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu			
560	565	570	
cga gaa tac ctc cga gcc cgg agg cca ccc ggg atg gag tac tcc tat			2378
Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr			
575	580	585	
gac att aac cgt gtt cct gag gag cag atg acc ttc aag gac ttg gtg			2426
Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val			
590	595	600	605
tca tgc acc tac cag ctg gcc aga ggc atg gag tac ttg gct tcc caa			2474
Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln			
610	615	620	
aaa tgt att cat cga gat tta gca gcc aga aat gtt ttg gta aca gaa			2522
Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu			
625	630	635	
aac aat gtg atg aaa ata gca gac ttt gga ctc gcc aga gat atc aac			2570
Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn			
640	645	650	
aat ata gac tat tac aaa aag acc acc aat ggg cgg ctt cca gtc aag			2618
Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys			
655	660	665	
tgg atg gct cca gaa gcc ctg ttt gat aga gta tac act cat cag agt			2666
Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser			
670	675	680	685
gat gtc tgg tcc ttc ggg gtg tta atg tgg gag atc ttc act tta ggg			2714
Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly			
690	695	700	
ggc tcg ccc tac cca ggg att ccc gtg gag gaa ctt ttt aag ctg ctg			2762
Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu			

705	710	715	
aag gaa gga cac aga atg gat aag cca gcc aac tgc acc aac gaa ctg			2810
Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu			
720	725	730	
tac atg atg atg agg gac tgt tgg cat gca gtg ccc tcc cag aga cca			2858
Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro			
735	740	745	
acg ttc aag cag ttg gta gaa gac ttg gat cga att ctc act ctc aca			2906
Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr			
750	755	760	765
acc aat gag gaa tac ttg gac ctc agc caa cct ctc gaa cag tat tca			2954
Thr Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser			
770	775	780	
cct agt tac cct gac aca aga agt tct tgt tct tca gga gat gat tct			3002
Pro Ser Tyr Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser			
785	790	795	
gtt ttt tct cca gac ccc atg cct tac gaa cca tgc ctt cct cag tat			3050
Val Phe Ser Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr			
800	805	810	
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Pro His Ile Asn Gly Ser Val Lys Thr			
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<211> 1541

<212> DNA

<213> Homo sapiens

<220>

<220>

<221> CDS

<222> (276)...(1040)

<400> 26

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cattgcgcgt agtccatgcc cgtagaggaa gtgtgcagat gggattaacg tccacatgga	240
gatatggaag aggaccgggg attggtaccg taacc atg gtc agc tgg ggt cgt	293
Met Val Ser Trp Gly Arg	
1 5	
ttc atc tgc ctg gtc gtg gtc acc atg gca acc ttg tcc ctg gcc cgg	341
Phe Ile Cys Leu Val Val Val Thr Met Ala Thr Leu Ser Leu Ala Arg	
10 15 20	
ccc tcc ttc agt tta gtt gag gat acc aca tta gag cca gaa gag cca	389
Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu Pro	
25 30 35	
cca acc aaa tac caa atc tct caa cca gaa gtg tac gtg gct gcg cca	437
Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala Pro	
40 45 50	
ggg gag tcg cta gag gtg cgc tgc ctg ttg aaa gat gcc gcc gtg atc	485
Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val Ile	
55 60 65 70	
agt tgg act aag gat ggg gtg cac ttg ggg ccc aac aat agg aca gtg	533
Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr Val	
75 80 85	
ctt att ggg gag tac ttg cag ata aag ggc gcc acg cct aga gac tcc	581
Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr Pro Arg Asp Ser	
90 95 100	
ggc ctc tat gct tgt act gcc agt agg act gta gac agt gaa act tgg	629
Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr Trp	
105 110 115	
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Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp Glu	
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<210> 28

<211> 2650

<212> DNA

<213> Homo sapiens

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